

Amendments to the Claims

Claim 1 (Currently amended): A method of genetically identifying a marker correlated with favorable muscle growth and/or meat quality in animals of a particular breed, strain, population, or group comprising:
obtaining a sample of genetic material from ~~said each~~ animal, said sample comprising a CKM gene;
assaying each sample for the presence of a polymorphic allele in ~~a~~said CKM gene; and
correlating whether a statistically significant association exists between said polymorphic allele and favorable muscle growth and/or favorable meat quality in ~~an each~~ animal, ~~of a particular breed, strain, population, or group~~ whereby ~~said each~~ animal can be characterized for said marker.

Claim 2 (Original): The method of claim 1 wherein said animal is a pig.

Claim 3 (Original): The method of claim 1 wherein said assaying is selected from the group consisting of: restriction fragment length polymorphism (RFLP), heteroduplex analysis, single-strand conformational polymorphism (SSCP), denaturing gradient gel electrophoresis (DGGE), single base extension, mass spectrometry, oligo ligation assay (ligase chain reaction), DNA sequencing and temperature gradient gel electrophoresis (TGGE).

Claim 4 (Original): The method of claim 1 further comprising amplifying an amount of said gene or a portion thereof which contains said polymorphism.

Claim 5 (Original): The method of claim 4 wherein said amplification includes selecting a forward a reverse primer capable of amplifying a region of said gene which contains at least one polymorphic site.

Claim 6 (Original): The method of claim 1 wherein said gene is the CKM gene.

Claim 7 (Original): The method of claim 6 wherein said gene contains a polymorphic MspAII site.

Claim 8 (Original): The method of claim 7 wherein said polymorphic site is amplified by primers selected from and based upon SEQ ID NO: 7 and SEQ ID NO: 8.

Claim 9 (Original): The method of claim 6 wherein said gene contains a polymorphic BamHI site.

Claim 10 (Original): The method of claim 9 wherein said polymorphic site is amplified by primers selected from and based upon SEQ ID NO: 9 and SEQ ID NO: 10.

Claim 11 (Original): The method of claim 6 wherein said gene contains a polymorphism identified by a 9 base pair insertion/deletion.

Claim 12 (Original): The method of claim 11 wherein said polymorphism is amplified by primers selected from and based upon SEQ ID NO: 11 and SEQ ID NO: 12.

Claim 13 (Withdrawn): The method of claim 1 wherein said gene is SCN4 α .

Claim 14 (Withdrawn): The method of claim 13 wherein said gene contains a polymorphic BsrI site.

Claim 15 (Withdrawn): The method of claim 14 wherein said polymorphic site is amplified by primers selected from and based upon SEQ ID NO: 13 and SEQ ID NO: 14.

Claim 16 (Withdrawn): The method of claim 13 wherein said gene contains a polymorphic PstI site.

Claim 17 (Withdrawn): The method of claim 16 wherein said polymorphic site is amplified by primers selected from and based upon SEQ ID NO: 15 and SEQ ID NO: 16.

Claim 18 (Withdrawn): The method of claim 13 wherein said gene contains a polymorphic SalI site.

Claim 19 (Withdrawn): The method of claim 18 wherein said polymorphic site is amplified by primers selected from and based upon SEQ ID NO: 17 and SEQ ID NO: 18.

Claim 20 (Withdrawn): The method of claim 1 wherein said gene is the LDH α gene.

Claim 21 (Withdrawn): The method of claim 20 wherein said gene contains a polymorphic AciI site.

Claim 22 (Withdrawn): The method of claim 21 wherein said polymorphic site is amplified by a forward and a reverse primer selected from and based upon SEQ ID NO: 19 and SEQ ID NO: 20.

Claim 23 (Original): The method of claim 7 wherein said polymorphic site is a C to T single nucleotide substitution in the 5' UTR region of said gene.

Claim 24 (Original): The method of claim 9 wherein said polymorphic site is a G to T single nucleotide substitution in intron 2 of said gene.

Claim 25 (Original): The method of claim 11 wherein said 9 base pair insertion/deletion is characterized by a nucleotide sequence -TGAGCTTCC- present in allele 1 but not present in allele 2.

Claim 26 (Withdrawn): The method of claim 14 wherein said polymorphic site is a C to G single nucleotide substitution in exon 24 of said gene.

Claim 27 (Withdrawn): The method of claim 16 wherein said polymorphic site is a G to A single nucleotide substitution in exon 11 of said gene.

Claim 28 (Withdrawn): The method of claim 18 wherein said polymorphic site is a G to A single nucleotide substitution in exon 2 of said gene.

Claim 29 (Withdrawn): The method of claim 20 wherein said polymorphic site is a polymorphic base, R, wherein said base is a G or an A in exon 5 of said gene.

Claim 30 (Currently Amended): A method of screening an animal to determine said animal's genetic potential for animal breeding comprising:
obtaining a genetic sample from said animal;
identifying said animal's genotype wherein said genotype has at least one polymorphic site in a gene CKM; and
making genetic assessments based upon the presence of an allele characterized by a
polymorphism in said gene which is correlated with favorable breeding traits.

Claim 31 (Previously presented): The method of claim 30 wherein identifying at least one polymorphic site comprises:
amplifying said sample which contains a polymorphism;
generating or destroying a restriction site in said sample;
determining whether a site is cleaved by a specific restriction endonuclease; and
determining whether said sample contains an insertion or deletion, wherein cleavage of a restriction endonuclease site or an insertion or deletion indicates the presence of a polymorphism.

Claim 32 (Original): The method of claim 31 further comprising running gel electrophoresis to identify polymorphism.

Claim 33 (Original): The method of claim 30 wherein said genotype is characterized by at least one polymorphism in the CKM gene.

Claim 34 (Original): The method of claim 33 wherein said polymorphism is identified by cleavage of a MspAII restriction endonuclease site in a region amplified by primers SEQ ID NO: 7 and SEQ ID NO: 8.

Claim 35 (Original): The method of claim 33 wherein said polymorphism is identified by cleavage of a BamHI restriction endonuclease site in a region amplified by primers SEQ ID NO: 9 and SEQ ID NO: 10.

Claim 36 (Original): The method of claim 33 wherein said polymorphism is identified by the presence or absence of a 9 base pair insertion/deletion in a region amplified by primers SEQ ID NO: 11 and SEQ ID NO: 12.

Claim 37 (Withdrawn): The method of claim 30 wherein said genotype is characterized by at least one polymorphic site in the SCN4 α gene.

Claim 38 (Withdrawn): The method of claim 37 wherein said polymorphism is identified by cleavage of a BsrI restriction endonuclease site in a region amplified by primers SEQ ID NO: 13 and SEQ ID NO: 14.

Claim 39 (Withdrawn): The method of claim 37 wherein said site is identified by cleavage of a PstI restriction endonuclease site in a region amplified by primers SEQ ID NO: 15 and SEQ ID NO: 16.

Claim 40 (Withdrawn): The method of claim 37 wherein said polymorphism is identified by cleavage of a SalI restriction endonuclease site in a region amplified by primers SEQ ID NO: 17 and SEQ ID NO: 18.

Claim 41 (Withdrawn): The method of claim 30 wherein said genotype is characterized by a polymorphism in the LDH α gene.

Claim 42 (Withdrawn): The method of claim 41 wherein said polymorphism is identified by cleavage of an AclI restriction endonuclease site in a region amplified by primers SEQ ID NO: 19 and SEQ ID NO: 20.

Claim 43 (Original): The method of claim 30 wherein said animal is a pig.

Claim 44 (Original): The method of claim 30 wherein said breeding traits comprises favorable meat quality, heavy muscling, and/or skeletal muscle cramping disease.

Claim 45 (Previously presented): A method of genotyping an animal comprising:
determining the alleles present in an animal said alleles comprising those which include one or more of the following polymorphic sites: a MspAII, BamHI, or a 9 bp insertion/deletion in a CKM gene, wherein the presence of one alternative of said polymorphic site is associated with favorable muscle growth and/or meat quality.

Claim 46 (Original): The method of claim 45 wherein said animal is a pig.

Claim 47 (Currently amended): A method of genotyping an animal at a polymorphic locus comprising:

obtaining a genetic sample from an animal;

assaying for the presence of an allele characterized by a polymorphism, said polymorphism characterized by the following:

- a) a polymorphism in the CKM gene said polymorphism located in the 5' untranslated ~~region~~ region of said gene as set forth in SEQ ID NO:1;
- b) a polymorphism in the CKM gene said polymorphism located in intron 2 of said gene as set forth in SEQ ID NO:2; or
- c) a polymorphism in the CKM gene said polymorphism characterized by a 9 bp insertion/deletion of the nucleotide sequence TGAGCTTCC in intron 2 of said gene as set forth in SEQ ID NO:2.

Claim 48 (Original): The method of claim 47 wherein said animal is a pig.

Claim 49 (Currently Amended): A method of detecting the presence of haplotypes which is predictive for determining the presence of a gene linked with favorable meat quality in an animal, said method comprising:

a) analyzing a sample of genetic material from said animal for polymorphisms in the gene CKM, wherein the presence of an allele characterized by said polymorphisms are associated with favorable meat quality traits and wherein said polymorphisms are selected from the group consisting of MspA1I and a 9 bp insertion/deletion; and

b) correlating the presence of said polymorphism with the presence of said haplotypes such that said haplotypes are detected.

Claim 50 (Original): The method of claim 49 wherein said haplotypes are 1-1, 1-2 and 2-2.

Claim 51 (Original): The method of claim 49 wherein said animal is a pig.